Amendments to the Claims

Please amend claims 1, 25, 44 and 60 as indicated in the listing of claims.

The listing of claims will replace all prior versions, and listings of claims in the application.

Listing of Claims:

1. (Currently amended) A set of primers, that selectively hybridize under highly stringent conditions to a nucleotide sequence ~~flanking and~~ within ~~fifty nucleotides of~~ one of the polycystic kidney disease-associated protein-1 (PKD1) gene sequences set forth as:

nucleotides 2043 to 4290 of SEQ ID NO:1,

nucleotides 17907 to 22489 of SEQ ID NO:1,

nucleotides 22218 to 26363 of SEQ ID NO:1,

nucleotides 26246 to 30615 of SEQ ID NO:1,

nucleotides 30606 to 33957 of SEQ ID NO:1,

nucleotides 36819 to 37140 of SEQ ID NO:1

nucleotides 37329 to 41258 of SEQ ID NO:1, and

nucleotides 41508 to 47320 of SEQ ID NO:1,

or to a nucleotide sequence complementary thereto,

wherein each of the primers comprises a 5' region and adjacent 3' region,

the 5' region comprising a nucleotide sequence that selectively hybridizes to a PKD1 gene sequence as set forth in SEQ ID NO:1, wherein the 5' region comprises at least ten contiguous nucleotides, and

the 3' region comprising a nucleotide sequence that selectively hybridizes to a PKD1 gene sequence as set forth in SEQ ID NO:1,

provided the primer does not consist of a sequence as set forth in SEQ ID NO:11, SEQ ID NO:18, SEQ ID NO:52, or SEQ ID NO:60;

wherein the primers amplify at least a first and a second amplification product, and wherein at least one of the primers for the first amplification product ~~includes at least~~ consists of SEQ ID NO: 3.

2. (Previously presented) The set of primers of claim 1,

wherein the 3' region comprises at least one 3' terminal nucleotide identical to a nucleotide that is 5' and adjacent to the nucleotide sequence of SEQ ID NO:1 to which the 5' region of the primer can hybridize, and

wherein said 3' terminal nucleotide is different from a nucleotide that is 5' and adjacent to a nucleotide sequence of the PKD1 homolog to which the 5' region of the primer can hybridize.

3. (Previously presented) The set of primers of claim 2, wherein the 3' region comprises 2 to 4 3' terminal nucleotides.

4. (Previously presented) The set of primers of claim 2, comprising a 5' region of 14 to 18 nucleotides and a 3' region of 2 to 6 nucleotides.

5.-15. (Canceled)

16. (Previously presented) A solid matrix, comprising the set of primers of claim 1, wherein each of the primers is immobilized on the solid matrix.

17. (Canceled)

18. (Withdrawn) The solid matrix of claim 17, wherein the matrix comprises a plurality of primers, wherein said primers are degenerate with respect to one or more codons encoding a polypeptide having an amino acid sequence as set forth in SEQ ID NO:2.

19. (Original) The solid matrix of claim 16, wherein the solid matrix is a microchip.

20.-24. (Canceled)

25. (Currently amended) A method of detecting the presence or absence of a mutation in a PKD1 polynucleotide in a sample, the method comprising:

contacting nucleic acid molecules in a sample with a first set of primer pairs to amplify a first amplification product, wherein at least one of the primers for the first amplification product ~~includes at least~~ consists of SEQ ID NO: 3, wherein the first set of primer pairs selectively hybridize under highly stringent conditions to a PKD1 polynucleotide comprising SEQ ID NO: 1; and

contacting the first amplification product with a second set of primer pairs to amplify a second amplification product, and wherein the second set of primer pairs selectively hybridize under highly stringent conditions to the first amplification product; and

identifying the presence or absence of a mutation in the second amplification product, thereby detecting the presence or absence of a mutation in the PKD1 polynucleotide in the sample, wherein the mutation is located at nucleotides 3110, 3336, 3707, 4168, 6078, 6089, 6326, 7205-7211, 7415, 7433, 7535-7536, 7883, 8159-8160, 8298, 9164, 9213, 9326 of SEQ ID NO:1, and wherein the presence of a mutation is indicative of a PKD1-associated disorder.

26.-27. (Canceled)

28. (Original) The method of claim 25, wherein amplification is performed by a polymerase chain reaction.

29. (Original) The method of claim 25, wherein the PKD1 polynucleotide is a variant PKD1 polynucleotide.

30. (Withdrawn) The method of claim 29, wherein the variant PKD1 polynucleotide comprises a nucleotide sequence substantially identical to SEQ ID NO:1, wherein nucleotide 474 is a T; nucleotide 487 is an A; nucleotide 4884 is an A; nucleotide 6058 is a T; nucleotide 6195 is n A; nucleotide 7376 is a C; nucleotide 7696 is a T; nucleotide 8021 is an A; nucleotide 9367 is a T; nucleotide 10143 is a G; nucleotide 10234 is a C; or nucleotide 10255 is a T.

31. (Previously presented) The method of claim 25, wherein identifying the presence or absence of a mutation in the second amplification product comprises determining the nucleotide sequence of the second amplification product.

32. (Previously presented) The method of claim 25, wherein identifying the presence or absence of a mutation in the second amplification product comprises determining the melting temperature of the second amplification product, and comparing the melting temperature to the melting temperature of a corresponding nucleotide sequence of SEQ ID NO:1.

33. (Previously presented) The method of claim 25, wherein identifying the presence or absence of a mutation in the second amplification product is performed using denaturing high performance liquid chromatography.

34. (Previously presented) The method of claim 25, wherein identifying the presence or absence of a mutation in the second amplification product is performed using matrix-assisted laser desorption time of flight mass spectrometry.

35. (Previously presented) The method of claim 25, wherein identifying the presence or absence of a mutation in the second amplification product is performed using high throughput conformation-sensitive gel electrophoresis.

36. (Previously presented) The method of claim 25, wherein identifying the presence or absence of a mutation in the second amplification product is performed by a method selected from single stranded conformation analysis, denaturing gradient gel electrophoresis, an RNAse protection assay, allele-specific oligonucleotide detection, an allele-specific polymerase chain reaction, and an oligonucleotide ligation assay.

37. (Previously presented) The method of claim 25, wherein identifying the presence or absence of a mutation in the second amplification product is performed using a primer extension reaction assay,

wherein the primer extension reaction is performed using a detectably labeled primer and a mixture of deoxynucleotides and dideoxynucleotides, and

wherein the primer and mixture are selected so as to enable differential extension of the primer in the presence of a wild type PKD1 polynucleotide as compared to a mutant PKD1 polynucleotide.

38. (Canceled).

39. (Original) The method of claim 25, wherein the method is performed in a high throughput format using a plurality of samples.

40. (Original) The method of claim 39, wherein plurality of samples are in an array.

41. (Original) The method of claim 40, wherein the array comprises a microtiter plate.

42. (Original) The method of claim 40, wherein the array is on a microchip.

43. (Cancelled)

44. (Currently amended) A method of identifying a subject at risk for autosomal dominant polycystic kidney disease (ADPKD), the method comprising:

contacting nucleic acid molecules in a sample from a subject with a set of primer pairs to amplify a first amplification product, wherein the sample is contacted with a first set of primer pairs, wherein at least one of the primers for the first amplification product ~~includes at least~~ consists of SEQ ID NO: 3, and the first amplification product is subsequently contacted with a second set of primer pairs to amplify a second amplification product, and wherein the primer pairs selectively hybridize to a PKD1 polynucleotide comprising SEQ ID NO: 1 and amplify a region of SEQ ID NO: 1 under conditions suitable for amplification of the PKD1 polynucleotide by the primer pair, thereby generating a first and second amplification product; and

detecting the presence or absence of a mutation indicative of ADPKD in the second amplification product,

wherein the mutation is located at nucleotides 3110, 3336, 3707, 4168, 6078, 6089, 6326, 7205-7211, 7415, 7433, 7535-7536, 7883, 8159-8160, 8298, 9164, 9213, 9326 of SEQ ID NO:1,

wherein the absence of the mutation identifies the subject is not at risk for ADPKD,

and wherein the presence of the mutation identifies the subject is at risk for ADPKD.

45.-47. (Canceled)

48. (Original) The method of claim 44, wherein the method is performed in a high throughput format.

49. (Previously presented) The method of claim 44, wherein detecting the presence or absence of a mutation indicative of ADPKD in the amplification product comprises accumulating data representative of the presence or absence of the mutation.

50. (Previously presented) The method of claim 49, wherein the data is formatted into a report indicating whether a subject is at risk for ADPKD.

51. (Original) The method of claim 50, further comprising transmitting the report to a user.

52. (Original) The method of claim 51, wherein transmitting the report comprises sending the report over the internet, by facsimile or by mail.

53.-54. (Canceled)

55. (Previously presented) The method of claim 44, detecting the presence or absence of the mutation comprises determining the nucleotide sequence of the amplification product, and comparing the nucleotide sequence to a corresponding nucleotide sequence of SEQ ID NO:1.

56. (Previously presented) The method of claim 44, wherein detecting the presence or absence of the mutation comprises determining the melting temperature of the amplification product, and comparing the melting temperature to the melting temperature of a corresponding nucleotide sequence of SEQ ID NO:1.

57. (Previously presented) The method of claim 44, wherein detecting the presence or absence of the mutation is performed using denaturing high performance liquid chromatography.

58. (Withdrawn) The method of claim 44, wherein the mutation indicative of a PKD1 associated disorder comprises a nucleotide sequence substantially identical to SEQ ID NO:1, wherein nucleotide 3110 is a C; nucleotide 8298 is a G; nucleotide 9164 is a G; nucleotide 9213 is an A; nucleotide 9326 is a T; or nucleotide 10064 is an A.

59. (Previously presented) The method of claim 44, wherein the mutation indicative of ADPKD comprises a nucleotide sequence substantially identical to SEQ ID NO:1, wherein nucleotide 3336 is deleted.

60. (Currently amended) A method of diagnosing an autosomal dominant polycystic kidney disease (ADPKD) in a subject, the method comprising:

amplifying a portion of a PKD1 gene in a nucleic acid sample from a subject with a first set of primer pairs, wherein at least one of the primers for the first amplification product ~~includes at least~~ consists of SEQ ID NO: 3, and wherein the primer pairs selectively hybridize to SEQ ID NO: 1 and amplify a region of SEQ ID NO: 1 to obtain a first amplification product;

amplifying the first amplification product with at least a second set of primer pairs to obtain a nested amplification product, and wherein the second set of primer pairs is suitable for performing nested amplification of the first amplification product; and

determining whether the nested amplification product has a mutation associated with ADPKD,

wherein the mutation is located at nucleotides 3110, 3336, 3707, 4168, 6078, 6089, 6326, 7205-7211, 7415, 7433, 7535-7536, 7883, 8159-8160, 8298, 9164, 9213, 9326 of SEQ ID NO:1, and

wherein the presence of a mutation associated with is indicative of ADPKD, thereby diagnosing ADPKD in the subject.

61. (Original) The method of claim 60, wherein the method is performed in a high throughput format using a plurality of nucleic acid samples.

62.-75. (Canceled)

76. (Previously presented) The method of claim 25 or 44, wherein prior to identifying the presence or absence of a mutation in the second amplification product, the second amplification product is serially diluted to remove genomic contamination.

77. (Canceled)

78. (Previously presented) The method of claim 60, wherein prior to obtaining the nested amplification product, the first amplification product is serially diluted to remove genomic contamination.

79. (Previously presented) The set of primers of claim 1, wherein the downstream primer for the first amplification product are selected from the group consisting of SEQ ID NOs: 4 and 6.

80. (Previously presented) The set of primers of claim 1, wherein the primers for the second amplification product are selected from the group consisting of SEQ ID NOs: 19, 20, 21, and 22.

81. (Previously presented) The method of claim 25, wherein the downstream primer for the first amplification product are selected from the group consisting of SEQ ID NOs: 4 and 6.

82. (Previously presented) The method of claim 25, wherein the primers for the second amplification product are selected from the group consisting of SEQ ID NOs: 19, 20, 21, and 22.

83. (Previously presented) The method of claim 44, wherein the downstream primer for the first amplification product are selected from the group consisting of SEQ ID NOs: 4 and 6.

84. (Previously presented) The method of claim 44, wherein the primers for the second amplification product are selected from the group consisting of SEQ ID NOs: 19, 20, 21, and 22.

85. (Previously presented) The method of claim 60, wherein the downstream primer for the first amplification product are selected from the group consisting of SEQ ID NOs: 4 and 6.

86. (Previously presented) The method of claim 60, wherein the primers for the second amplification product are selected from the group consisting of SEQ ID NOs: 19, 20, 21, and 22.